## SEQUENCE LISTING

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<110> McCall, Catherine A.
      Tang, Liang
      Heska Corporation
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<140> not yet assigned
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<150> 60/195,659
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	acg Thr												399
	tat Tyr										_		447
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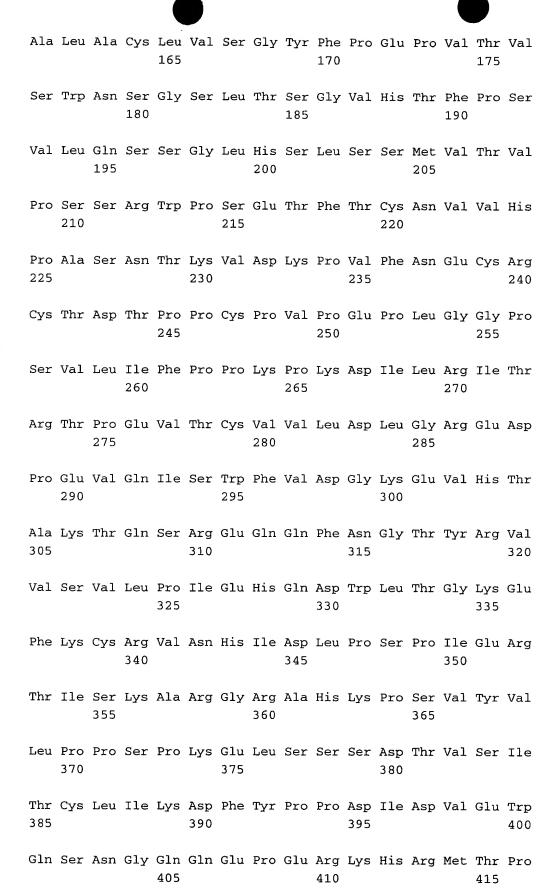
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Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly
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His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
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Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly 325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile 340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val 355 360 365

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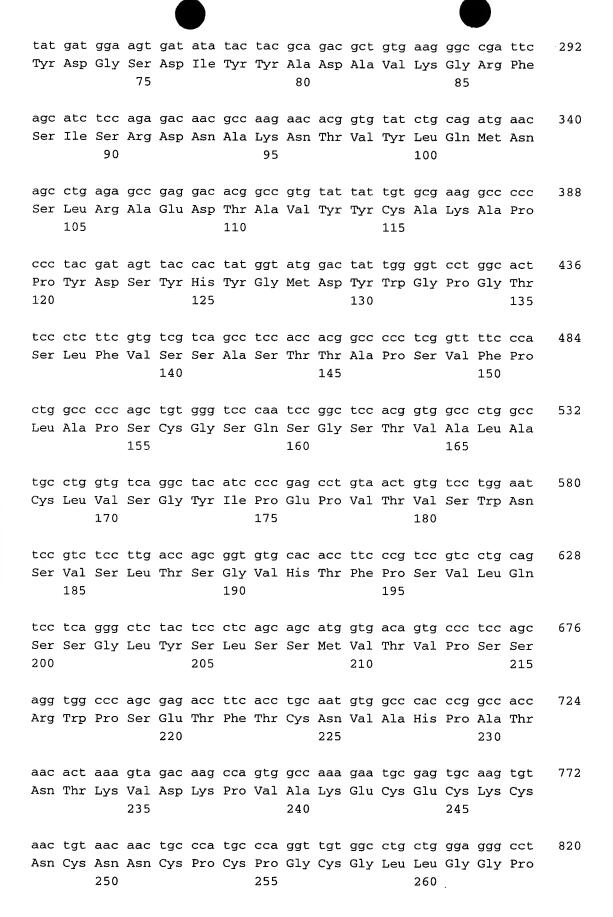
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                             15
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65



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	gag Glu											_			964
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	aat Asn												_		1300
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<213> Canis familiaris

<223> At location 27, n = unknown

<400> 17

Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Gly Asp Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe 35 40 45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Pro 50 55 60

Gln Trp Val Ala Thr Ile Arg Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala 65 70 75 80

Asp Ala Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn 85 90 95

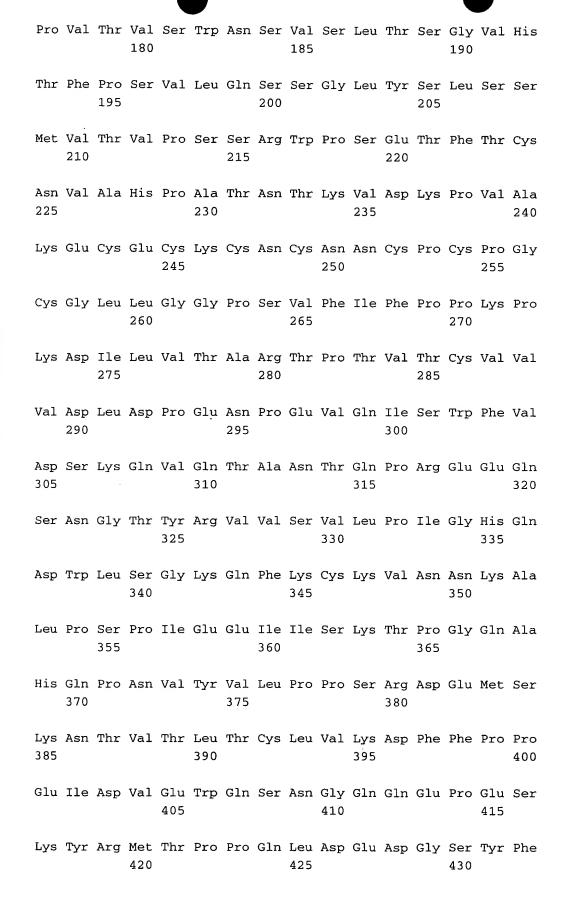
Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 100 105 110

Tyr Tyr Cys Ala Lys Ala Pro Pro Tyr Asp Ser Tyr His Tyr Gly Met 115 120 125

Asp Tyr Trp Gly Pro Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr 130 135 140

Thr Ala Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Gln Ser 145 150 155 160

Gly Ser Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Ile Pro Glu 165 170 175



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Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp 435 Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
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450 455 460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys 465 470

<211> 1456 <212> DNA <213> Canis familiaris <220> <223> At location 1430, n = unknown

<400> 18

<210> 18

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catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggetcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcaq 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg gagatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccaqtcctq 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaqqc cctcccaqca qqccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgtc 720
tactttagtg ttggtggccg ggtgggccac attgcaggtg aaggtctcgc tgggccacct 780
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cgggaaggtg tgcacaccgc tggtcaagga gacggaattc caggacacag ttacaggctc 900
ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggacccaca 960
gctgggggcc agtgggaaaa ccgagggggc cgtggtggag gctgacgaca cgaagaggga 1020
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acaataatac acggccgtgt cctcggctct caggctgttc atctgcagat acaccgtgtt 1140
cttggcgttg tctctggaga tgctgaatcg gcccttcaca gcgtctgcgt agtatatatc 1200
acttccatca taccgaatag ttgcgaccca ctgaggcccc ttccctggag actgacggac 1260
ccagctcatg gcacagctac taaaggtgaa tccagaggcc acacaggaca gtctcaagga 1320
cccccaggc ttcaccaggt ctcccccaga ctccaccagc tgcacgtcac cctggacacc 1380
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<210> 19

<211> 1453 <212> DNA <213> Canis far	miliaris		
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		ggt gag gta cgt ttg Gly Glu Val Arg Leu 20	100
		ggg tcc ctg aaa ctc Gly Ser Leu Lys Leu 35	148
		tac tcc atg gac tgg Tyr Ser Met Asp Trp 55	196
		gtc gcc ggg att aac Val Ala Gly Ile Asn 70	244
	Gly Thr Ser T	gtg aag ggc cga ttc Val Lys Gly Arg Phe 85	292
	g Asp Asn Ala L	tat ctg cag ata aac Tyr Leu Gln Ile Asn 100	340
		tgt gcc aag agc tgg Cys Ala Lys Ser Trp 115	388
		gga acc ctg gtc acc Gly Thr Leu Val Thr 135	436
		ttc cca ctg gcc ccc Phe Pro Leu Ala Pro 150	484

		ggg Gly							_	_	-	-		532
		tac Tyr 170												580
		agc Ser												628
		tcc Ser												676
		acc Thr												724
	-	aag Lys			-	_		~~	~	_				772
		tgt Cys 250												820
-		atc Ile		_		-	-			_		_	-	868
		gag Glu												916
		cag Gln					_	_	_	_			_	964
		cag Gln												1012
		ctc Leu 330					_		_		_	_		1060

acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr	
345 350 355	
atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg	
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu 360 365 370 375	
360 365 370 375	1
ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc	1204
Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys	
380 385 390	
ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc	1252
Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser	
395 400 405	
aat gga cag cag gag.cct gag agc aag tac cgc acg acc ccg ccc cag	1300
Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln	ı
410 415 420	
ctg gac gag gac ggg tec tac tte etg tac age aag ete tet gtg gae	1348
Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp	ı
425 430 435	
aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat	1396
Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His	
440 445 450 455	
gaa get eta eac aac eac tae aca eag gaa tee ete tee eat tet eeg	1444
Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro	
460 465 470	
ggt aaa tga	1453
Gly Lys	2.23
<210> 20	
<211> 473	
<212> PRT	
<213> Canis familiaris	
<400> 20	
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Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys	
20 25 30	

Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe 35 40 45

Arg Arg Tyr Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Ser Leu 50 55 60

Gln Trp Val Ala Gly Ile Asn Gly Asp Gly Thr Gly Thr Ser Tyr Ser 65 70 75 80

Gln Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 85 90 95

Thr Leu Tyr Leu Gln Ile Asn Ser Leu Arg Ala Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Ser Trp Ser Arg Asn Gly Asp Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro 130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr 145 150 155 160

Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr
165 170 175

Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro 180 185 190

Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr 195 200 205

Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala 210 215 220

His Pro Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu 225 230 235 240

Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro
245 250 255

Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys 260 265 270

Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val 275 280 285

Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp 290 295 300

Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe 305 310 315 320

Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp 325 330 335

Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu 340 345 350

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His 355 360 365

Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys 370 375 380

Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp 385 390 395 400

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys
405 410 415

Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu 420 425 430

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr 435 440 445

Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 450 455 460

Glu Ser Leu Ser His Ser Pro Gly Lys 465 470

<210> 21

<211> 1453

<212> DNA

<213> Canis familiaris

<400> 21

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tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg gagatggtcc tctcgatcgg 360
ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttccccttga gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgagggag tagagccctg aggactgcaq 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
aggctcgggg aagtagcctg acaccaggca ggccagggcc accgtggagc cggaagtgga 960
cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
gaccagggtt ccctggcccc agtagtcaag atccccatta cgagaccagc tcttggcaca 1080
ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga gggtgttctt 1140
ggcgttgtct ctggagatgg tgaatcggcc cttcacagtc tgtgaatagg atgttcctgt 1200
gccatcaccg ttaatcccgg cgacccactg caggctcttg cctggagcct ggcggaccca 1260
gtccatggag tatcttctga aggtgaatcc agaggccaca caagagagtt tcagggaccc 1320
cccaggette accaggette etccagaete caccaaacgt accteaccet ggacacettt 1380
taaaatagtg acaaggaaaa cccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtcctgagc act
                                                                   1453
<210> 22
<211> 66
<212> DNA
<213> Canis familiaris
<220>
<221> CDS
<222> (1)..(66)
<400> 22
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                                                                   48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
  1
                                     10
                                                         15
                                                                   66
tgc cca gcc cct gaa atg
Cys Pro Ala Pro Glu Met
             20
<210> 23
<211> 22
<212> PRT
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<213> Canis familiaris

<400> 23

F	ro 1	Lys	Arg	Glu	Asn 5	Gly	Arg	Val	Pro	Arg 10	Pro	Pro	Asp	Cys	Pro 15	Lys	
C	'ys	Pro	Ala	Pro 20	Glu	Met											
<	211	)> 2 .> 6 !> D:	6 NA	fam:	ilia	ris											
C				gctg	ggcat	it tọ	ggga	caato	c agg	gtgg	gcga	ggaa	actci	ttc (	catti	tctct	60 66
<	211 212	)> 2  > 9  > D   > C	38 NA	fam	iliaı	cis											
<		.> C		. (75	3)												
	220 223		t lo	catio	on 47	75, r	1 = i	ınkno	own								
		> 2! .cga		taaa	cagaa	ag go	cagga	atcaa	a tca	agtg					atg Met 5		54
					ctc Leu												102
					ttg Leu												150

45

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata

Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile

50

					_									_		
												gcc Ala				246
	_											cct Pro				294
												atc Ile				342
												gtt Val 115				390
												act Thr				438
_		-	-			_	_				_	ncc Xaa	_	-		486
			_		_	_		_		_		atc Ile	_	_		534
												ggc Gly			_	582
	_		_				_			_	_	agc Ser 195			~	630
									_		_	aag Lys				678
												agc Ser				726
				ccc Pro 235					tagg	gttco	ccg a	atgco	cccc	cg		773

- <210> 26
- <211> 239
- <212> PRT
- <213> Canis familiaris
- <223> At location 475, n = unknown
- <400> 26
- Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Thr Leu Leu Ala
  1 5 10 15
- His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser 20 25 30
- Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp 35 40 45
- Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro
  50 55 60
- Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser 65 70 75 80
- Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Gly Asn Ser Gly Thr
  85 90 95
- Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
  100 105 110
- Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr 115 120 125
- Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu 130 135 140
- Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys 165 170 175
- Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser

180 185 190

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr 195 200 205

Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His 210 215 220

Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser 225 230 235

<210> 27

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<223> At location 464, n = unknown

<400> 27

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<210> 28

<211> 578

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(423)

<220																
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<400	)> 28	3														
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	Gln	Asp	Trp		Asn	Gly	Lys	Glu		Lys	Cys	Arg	Val		His	
1				5					10					15		
ata	gac	ctc	ccg	tct	ccc	atc	gag	agg	acc	atc	tct	aag	gcc	aga	ggg	96
Ile	Asp	Leu	Pro	Ser	Pro	Ile	Glu		Thr	Ile	Ser	Lys		Arg	Gly	
			20					25					30			
			aag						_	_				-		144
Arg	Ala		Lys	Pro	Ser	Val		Val	Leu	Pro	Pro		Pro	Lys	Glu	
		35					40					45				
ttg	tca	tcc	agt	gac	aca	gtc	agc	atc	acc	tgc	ctg	ata	aaa	gac	ttc	192
Leu		Ser	Ser	Asp	Thr		Ser	Ile	Thr	Cys		Ile	Lys	Asp	Phe	
	50					55					60					
tac	cca	cct	gac	att	gat	gtg	gag	tgg	cag	agc	aat	gga	cag	cag	gag	240
	Pro	Pro	Asp	Ile	Asp	Val	Glu	Trp	Gln	Ser	Asn	Gly	Gln	Gln	Glu	
65					70					75					80	
cct	gag	agc	aag	tac	cgc	acg	acc	ccg	ccc	cag	ctg	gac	gag	gac	ggg	288
Pro	Glu	Ser	Lys	Tyr	Arg	Thr	Thr	Pro	Pro	Gln	Leu	Asp	Glu	Asp	Gly	
				85					90					95		
tcc	tac	ttc	ctg	tac	agc	aag	ctc	tct	gtg	gac	aag	agc	cgc	tgg	cag	336
Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu		Val	Asp	Lys	Ser		Trp	Gln	
			100					105					110			
cgg	gga	gac	acc	ttc	ata	tgt	gcg	gtg	atg	cat	gaa	gct	cta	cac	aac	384
Arg	Gly		Thr	Phe	Ile	Cys		Val	Met	His	Glu		Leu	His	Asn	
		115					120					125				
cac	tac	aca	cag	aaa	tcc	ctc	tcc	cat	tct	ccg	ggt	aaa	tga	gcaa	cac	433
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	His	Ser	Pro	Gly	Lys				
	130					135					140					
gcco	eggea	acc o	cagca	aagco	cc c	ccaco	cctt	g gct	ctca	anga	tcc	ctgar	nga (	cacci	gagcc	493
cata	ttcc	·+~ ·	-ata	-ete-		1+000	rtano		7007	-02+	<b>~</b> ~ ~ ~ ·	a t a a a	200	2000	ancact	EEO
دددر	,	.cg (	Jycac	Jacac	4C C(	- cyyg	, cang	, cat	ccal	Luat	yaa	alddi	age a	accc	ancact	553
gcc	ctggg	jcc (	cttgo	caaaa	aa aa	aaaa										578

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<210> 29
<211> 141
<212> PRT
<213> Can
<223> At
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<213> Canis familiaris

<223> At locations 471, 481, 522 and 549, n = unknown

<400> 29

His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His

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Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
20 25 30

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu 35 40 45

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe 50 55 60

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Glu 65 70 75 80

Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly 85 90 95

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
100 105 110

Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn 115 120 125

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys 130 135 140

<210> 30

<211> 578

<212> DNA

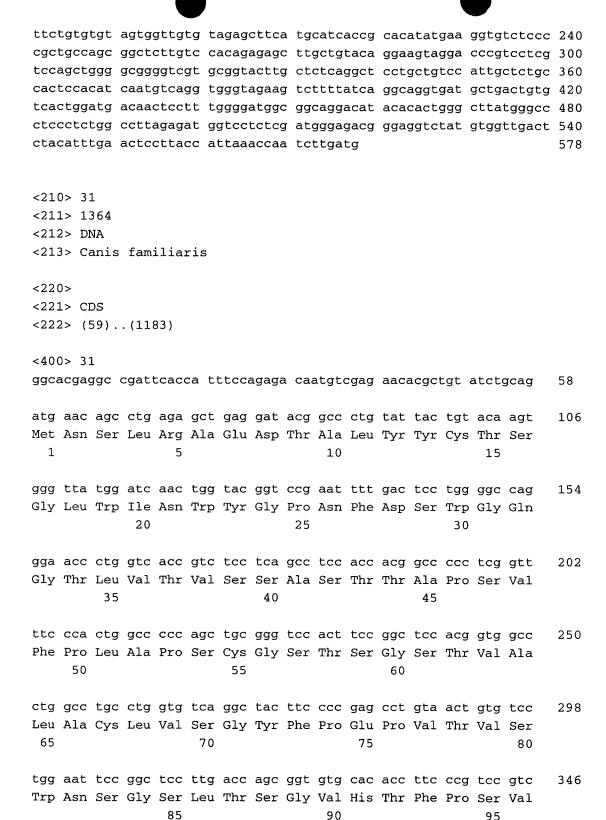
<213> Canis familiaris

<220>

<223> At locations 30, 57, 98 and 108, n = unknown

<400> 30

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ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro

105

394

		agc Ser					_		_	442
		gta Val					_			490
		cct Pro 150							_	538
		gtc Val					-	_		586
		aca Thr						_	_	634
		gag Glu							_	682
		aag Lys								730
		agt Ser 230				_	_			778
		acg Thr				_				826
		atc Ile								874
		ccg Pro								922
		ctg Leu							-	970

						aat Asn 310							_	_		-	1018
						ctg Leu	_		-					_		•	1066
						aag Lys											1114
						gaa Glu								_			1162
						ggt Gly		tgaç	gcaad	cac g	acccõ	ggcad	CC C	agcaa	agcco	:	1213
cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa													1273				
ccccgggtag gcacctggca tgaaataaag cacccagtac tgccctggaa aaaaaaaaaa													1333				
aaaaaaaaa aaaaaaaaaa a														1364			
<210> 32 <211> 375 <212> PRT <213> Canis familiaris																	
	<400	)> 32	)														
				Leu	Arg 5	Ala	Glu	Asp	Thr	Ala 10	Leu	Tyr	Tyr	Cys	Thr 15	Ser	
•	Gly	Leu	Trp	Ile 20	Asn	Trp	Tyr	Gly	Pro 25	Asn	Phe	Asp	Ser	Trp 30	Gly	Gln	
4	Gly	Thr	Leu 35	Val	Thr	Val	Ser	Ser 40	Ala	Ser	Thr	Thr	Ala 45	Pro	Ser	Val	
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85   90   95	
Low Thurs Low Clay Mote Core Core Low Live Ale Clay Arm The Ale The Three	
Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr  100 105 110	
103	
His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His	
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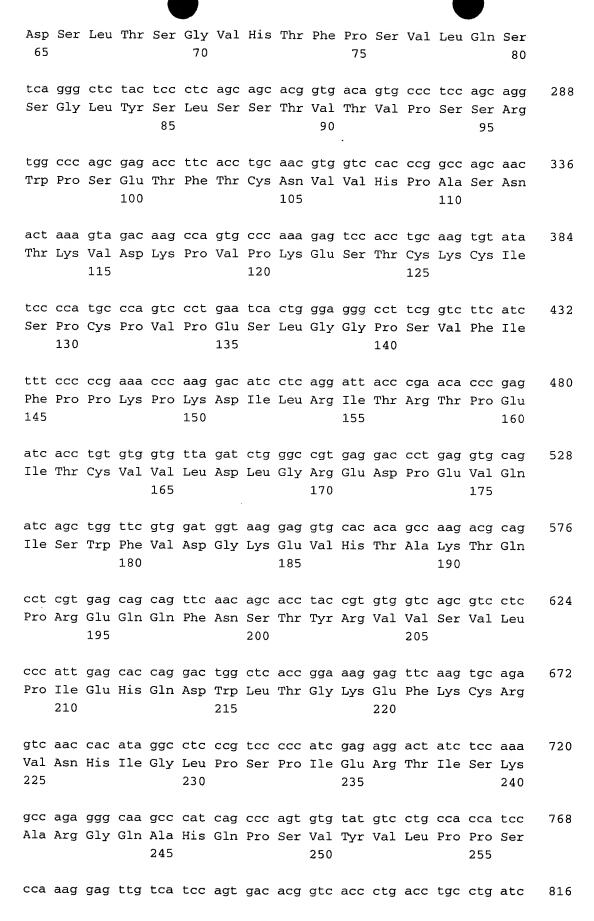
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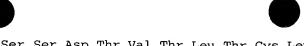
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Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys 

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser 

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile 

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly 

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp 

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser 

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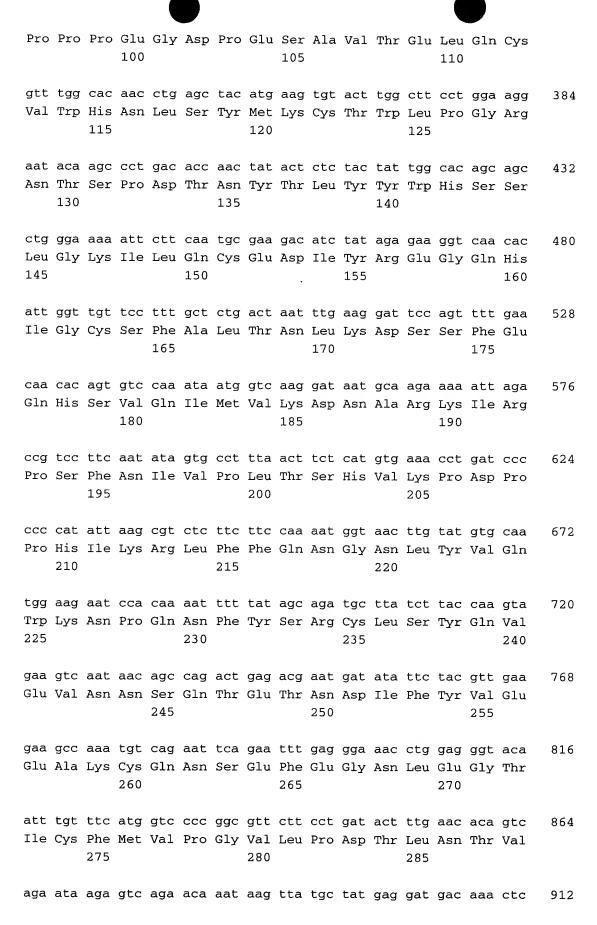
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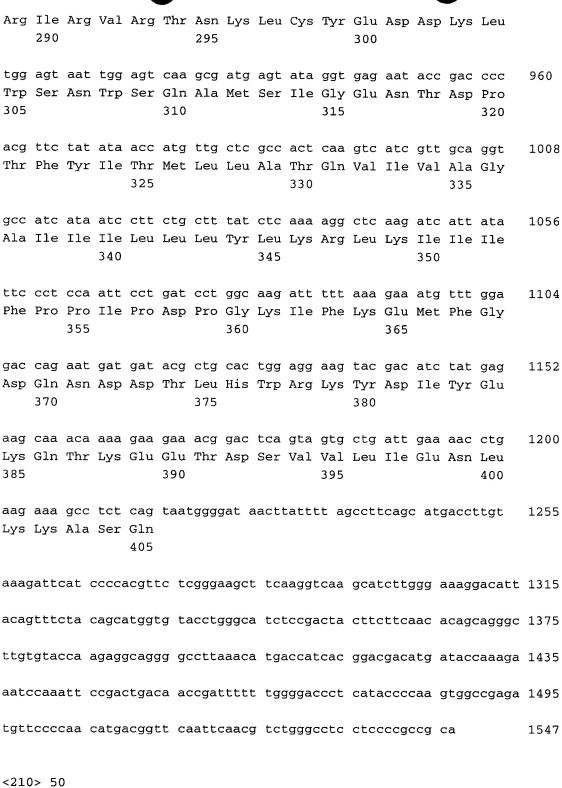
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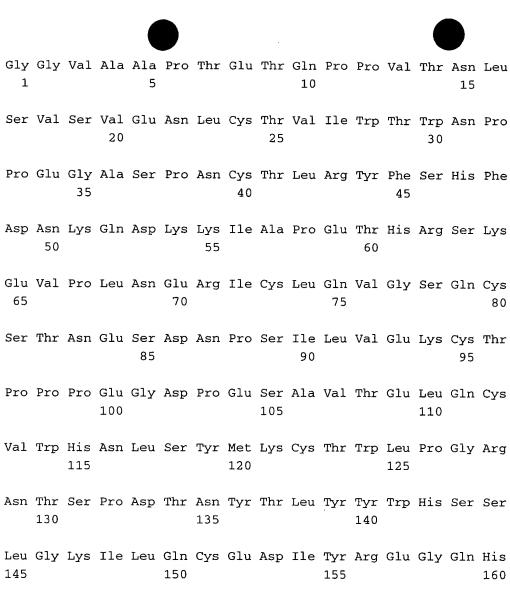
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Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val

Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu

235

250

240

255

230

245

Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr 260 265 270

Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val 275 280 285

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu 290 295 300

Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro 305 310 315 320

Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly 325 330 335

Ala Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile 340 345 350

Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly 355 360 365

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<213> Canis familiaris

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<400> 52

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accttacggt attttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgtc tgcaagtggg gtcccagtgc 240
agcaccaatg aaagtgacaa tcctagcatt ttggtggaaa agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttcctgg aaggaataca agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattettcaa tgcgaagaca tetatagaga aggtcaacac 480
attggttgtt cctttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt ccttcaatat agtgccttta 600
acttctcatg tgaaacctga tccccccat attaagcgtc tcttcttcca aaatggtaac 660
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gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
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<210> 53

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ttetttaaaa atettgeeag gateaggaat tggagggaat ataatgatet tgageetttt 180
gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240
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ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360
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aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtctg 480
gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540
ccattgcaca tacaagttac cattttggaa gaagagacgc ttaatatggg ggggatcagg 600
tttcacatga gaagttaaag gcactatatt gaaggacggt ctaatttttc ttqcattatc 660
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caggctgctg tgccaatagt agagagtata gttggtgtca gggcttgtat tccttccagg 840
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taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180
gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt
                                                                  228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
     1
                      5
                                         10
                                                             15
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	tgc Cys															276
	cct Pro															324
	tct Ser													-	_	372
	aca Thr 65															420
	aag Lys														_	468
	aac Asn													_		516
	aca Thr															564
	aca Thr														-	612
tgt Cys	gta Val 145	ta														620
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	)> 55 Ala		Ile	His 5	Leu	Asp	Val	Gly	Phe 10	Leu	Tyr	Thr	Leu	Leu 15	Val	
Cys	Thr	Ala	Phe 20	Gly	Ser	Met	Leu	Ser 25	Asn	Ala	Glu	Ile	Lys 30	Val	Asn	

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu 35 40 45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys 50 55 60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65 70 75 80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu 85 90 95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys 100 105 110

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Val 145

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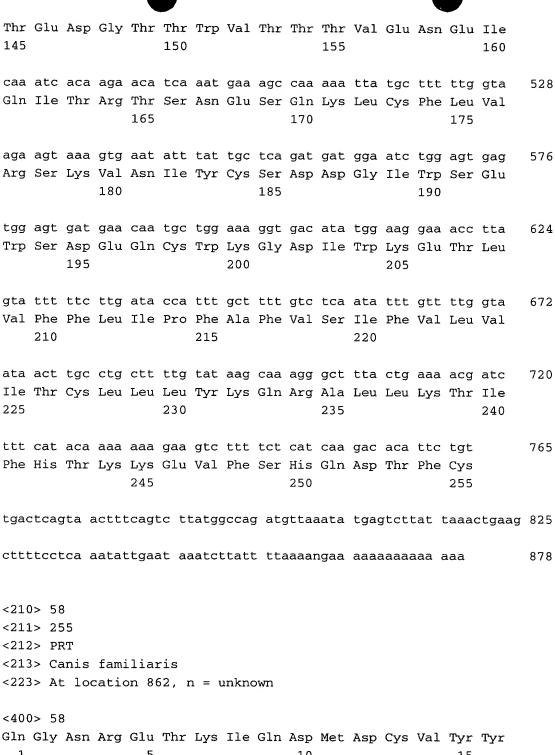
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<400> 56

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<210> 57 <211> 878

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	1> CI	os 1)	(765)	)												
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				gaa Glu 5												48
				tta Leu								_		-		96
				tac Tyr												144
				act Thr										_		192
				tat Tyr												240
				tca Ser 85							_		_			288
				caa Gln									_			336
				aag Lys												384
				att Ile												432
aca	gag	gat	ggt	act	act	tgg	gtg	act	acc	aca	gtt	gag	aat	gag	ata	480



Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly 50 55 60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile 65 70 75 80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe 85 90 95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
100 105 110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met 115 120 125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe 130 135 140

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val 165 170 175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu 180 185 190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu 195 200 205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val 210 215 220

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<212> DNA

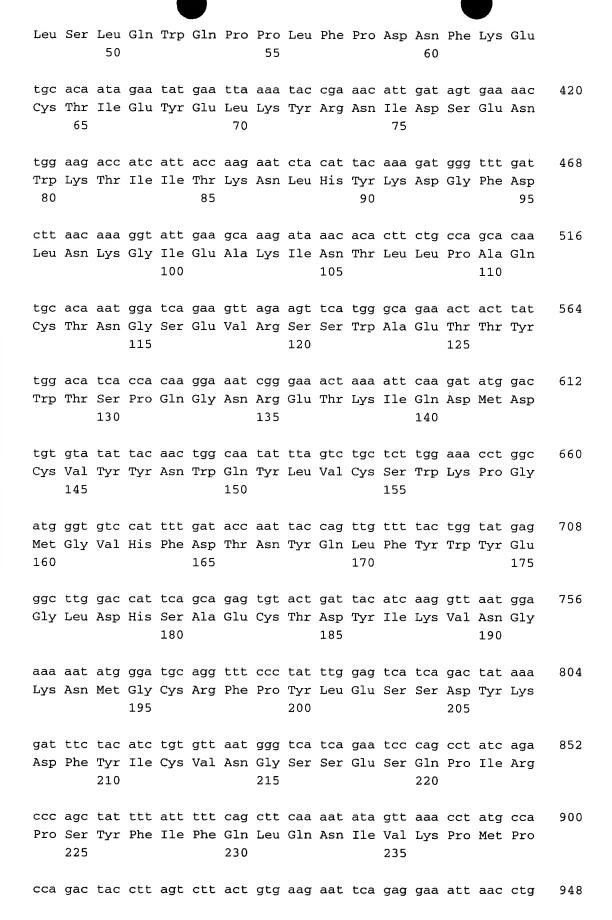
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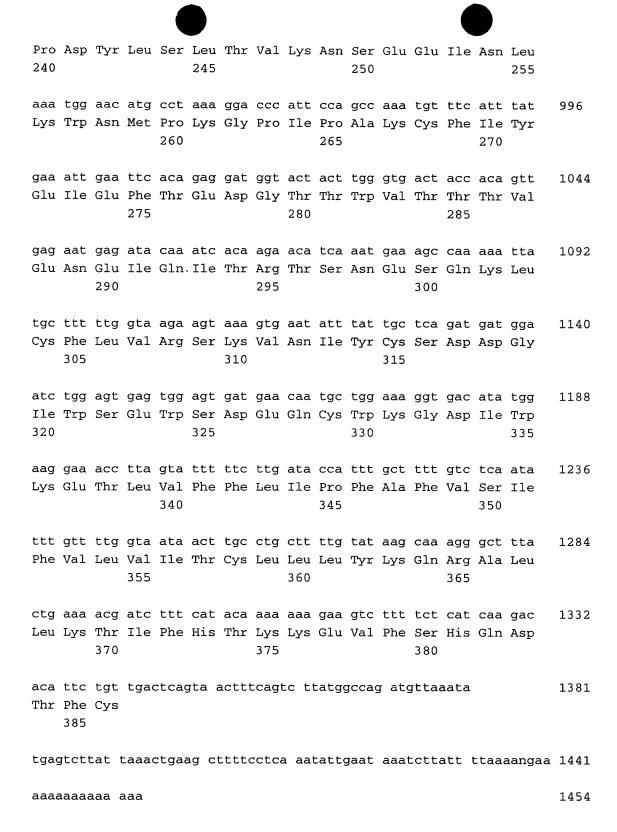
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<212> DNA
<213> Canis familiaris
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<221> CDS
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taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180
gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt
                                                                   228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
      1
                      5
                                         10
                                                              15
gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt
                                                                   276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
                 20
                                     25
                                                          30
aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat
                                                                   324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
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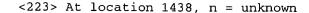


<210> 61

<211> 386

<212> PRT

<213> Canis familiaris



<400> 61

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Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn 20 25 30

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu 35 40 45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys 50 55 60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65 70 75 80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu 85 90 95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys 100 105 110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
115 120 125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
130 135 140

Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met 145 150 155 160

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly
165 170 175

Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys
180 185 190

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp 195 200 205

Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro 210 215 220

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro 225 230 235 240

Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys 245 250 255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu 260 265 270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu 275 280 285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys 290 295 300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile 305 310 315 320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys 325 330 335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe 340 345 350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu 355 360 365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr 370 380

Phe Cys 385

<210> 62

<211> 1454

<212> DNA

<213> Canis familiaris

<220>

<223> At location 17, n = unknown

<400> 62

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ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactetg etgaatggte caageeetea taccagtaaa acaactggta attggtatea 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
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cattccttaa aattatccgg aaataatgga ggttgccatt gcaaagagag ataacctaaa 1140
tatccagggt ccactatete aaaateetga ggaggattaa ettttatete ageatttgaa 1200
agcatagage caaatgetgt geaaacaage agggtataga ggaateegae atecaaatga 1260
atgaaagcca ttcctccaag attcaatact ttgaagtttc cactcaataa tatggtttct 1320
caagaaatga attatcatag gcaattatca caggtcctct tttttttctc ttctccagtt 1380
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<210> 63 <211> 1158 <212> DNA <213> Canis familiaris

<400> 63

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<212> DNA
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aaatggtatc aagaaaaata ctaaggtttc cttccatatg tcacctttcc agcattgttc 180
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caaaaagcat aatttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
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atagtetgat gactecaaat agggaaacet geateceata tittiteeat taacetigat 600
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ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 720
atatacacag tecatatett gaattttagt tteeegattt eettgtggtg atgteeaata 780
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tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 900
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                  5
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                                                         15
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Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
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                                 25
                                                     30
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Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu
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												att Ile		240
_												tca Ser 95	_	288
												caa Gln		336
												aac Asn		384
												ttt Phe	_	432
												tca Ser	_	480
		-			_	_					_	 tgc Cys 175		528
		_				-			_			tgt Cys	-	576
			_		_			_		_		att Ile		624
				_			_			_		agt Ser		672

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Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys

720

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			atc tgg agt gag Ile Trp Ser Glu 300	
			aag gaa acc tta Lys Glu Thr Leu 315	_
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aca aaa aaa gaa Thr Lys Lys Glu 355				1095
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Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

35 40 45

Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
50 55 60

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
65 70 75 80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu 85 90 95

Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
100 105 110

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp 115 120 125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp 130 135 140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala 145 150 155 160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg 165 170 175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val 180 185 190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe 195 200 205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu 210 215 220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys 225 230 235 240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu 245 250 255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile 260 265 270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser 275 280 285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser

290 295 300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe 305 310 315 320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr 325 330 335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His  $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350$ 

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<211> 1095

<212> DNA

<213> Canis familiaris

<400> 67

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<210> 68

<211> 954

<212> DNA

<213> Canis familiaris

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. 404	0. (															
	0> 68															
														cag		48
	Ser	Met	Leu		Asn	Ala	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	
1				5					10					15		
														caa		96
Phe	Glu	Ile		Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp	
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caa	cct	cca	tta	ttt	ccg	gat	aat	ttt	aag	gaa	tgc	aca	ata	gaa	tat	144
Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr	
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Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile	
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Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	
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Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser	
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gga	aat	cgg	gaa	act	aaa	att	caa	gat	atg	gac	tgt	gta	tat	tac	aac	384
Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	
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gat	acc	aat	tac	caq	t.t.a	ttt	tac	t.aa	tat	gag	aac	t.t.a	gac	cat	tca	480
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145			-1-		150		-1-		-1-	155	0-1			*****	160	
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gca	gag	tat	act	gat	tac	atc	aag	att	aat	aas	222	aat	ato	gga	tac	528
_													_	Gly	-	220
=4	Jau	-	- 111	165	- X -	E	Lys	vul	170	<b>υ</b> ±χ	בעב	11011	13C L	175	Cys	
				.03					110					1/3		

			ccc Pro									-				_	576
	_		ggg Gly 195			_		_			_						624
			ctt Leu							_			_			-	672
]			gtg Val	_				_			_				_		720
			ccc Pro					_				_		~			768
			ggt Gly														816
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<213> Canis familiaris

<400> 69

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp

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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser 145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile 195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser 210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro 225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln 260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg

275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp 290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr 305 310 315

<210> 70

<211> 954

<212> DNA

<213> Canis familiaris

<400> 70

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<211> 1686

<212> DNA

<213> Canis familiaris

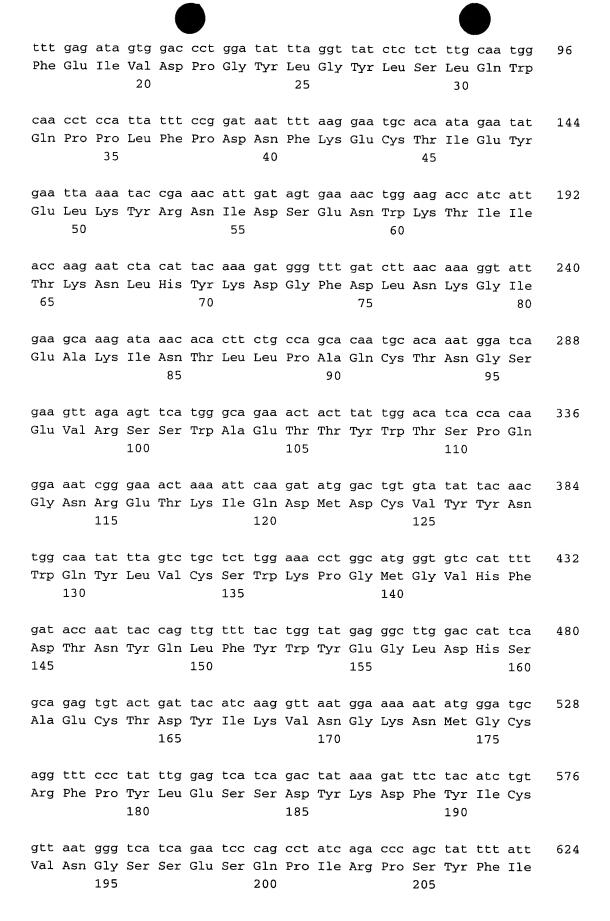
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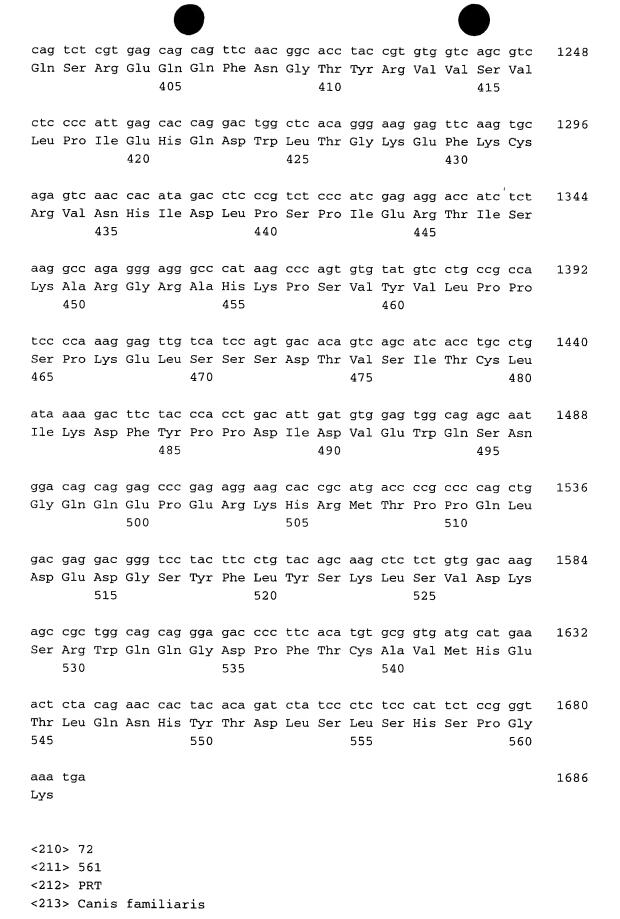
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										cca Pro 220	-			_	672
						_			_	aaa Lys	~ ~		_		720
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										tgc Cys				-	864
					_		_	_		atc Ile 300		_			912
							-			aag Lys	_				960
		_	_	_					_	tgc Cys	_	_		•	1008
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<400> 72

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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser 145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys 180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile 195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser 210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro 225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr

245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro 

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn 485 490 495

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu

Gly Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu

500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys 515 520 525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu 530 540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly 545 550 555 560

Lys

<210> 73 <211> 1686 <212> DNA

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

10

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr 35 40 45

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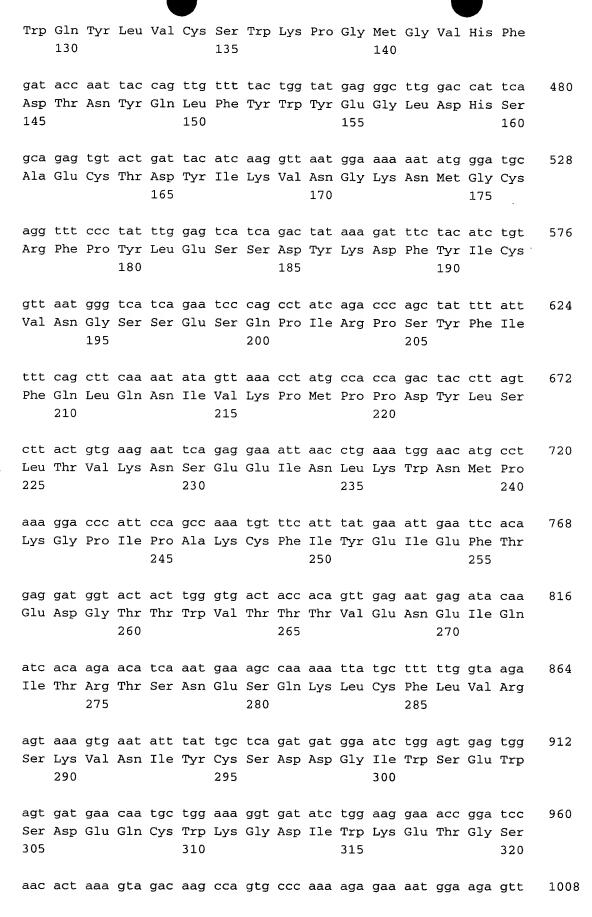
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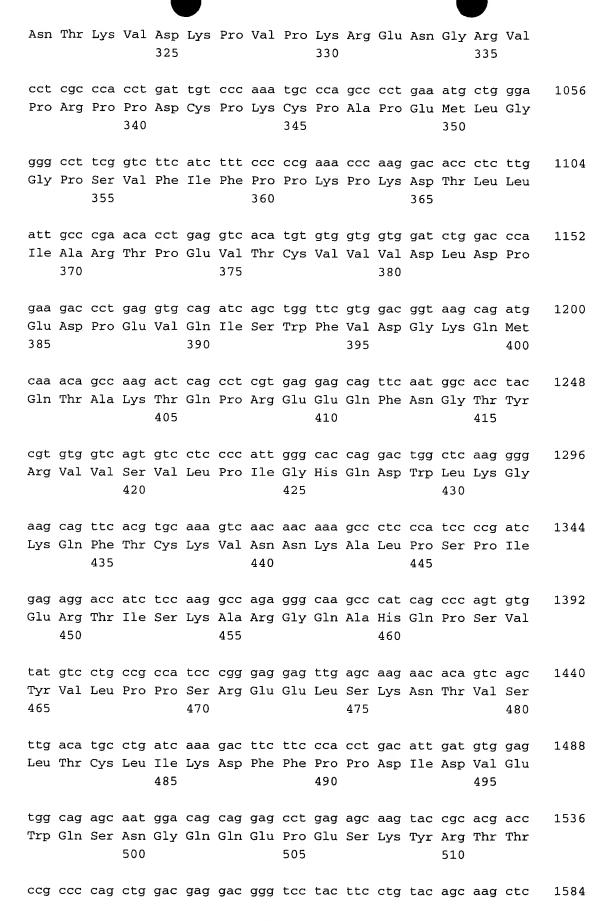
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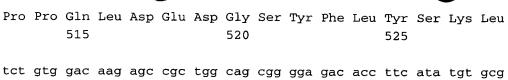
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tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432







Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala 530 535 540

gtg atg cat gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc 1680 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser 545 550 555 560

cat tct ccg ggt aaa tga 1698 His Ser Pro Gly Lys 565

<210> 75 <211> 565 <212> PRT <213> Canis familiaris

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met 

Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
405
410
415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
420 425 430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile 435 440 445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val 450 455 460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser 465 470 475 480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu 485 490 495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr 500 505 510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu 515 520 525

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His Ser Pro Gly Lys 565

<210> 76

<211> 1698

<212> DNA

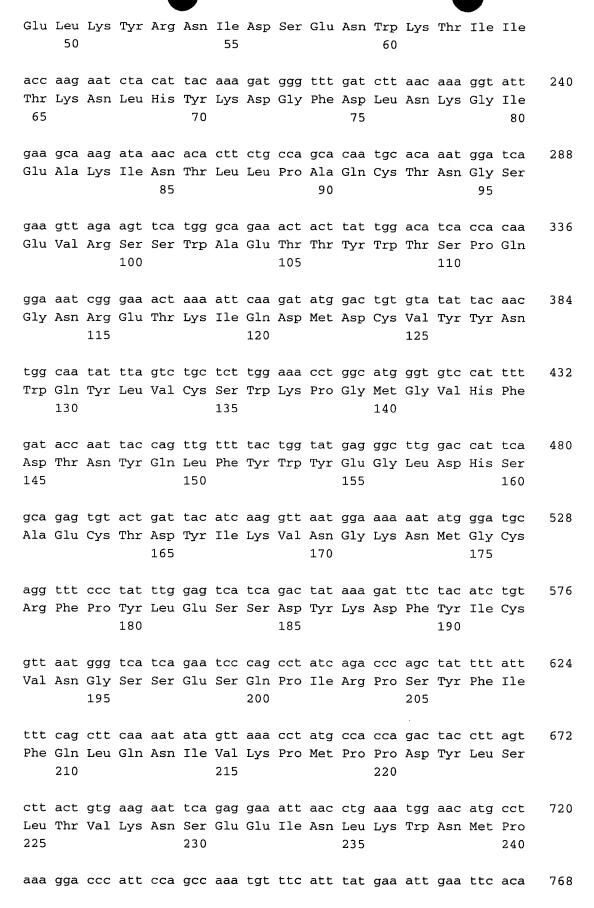
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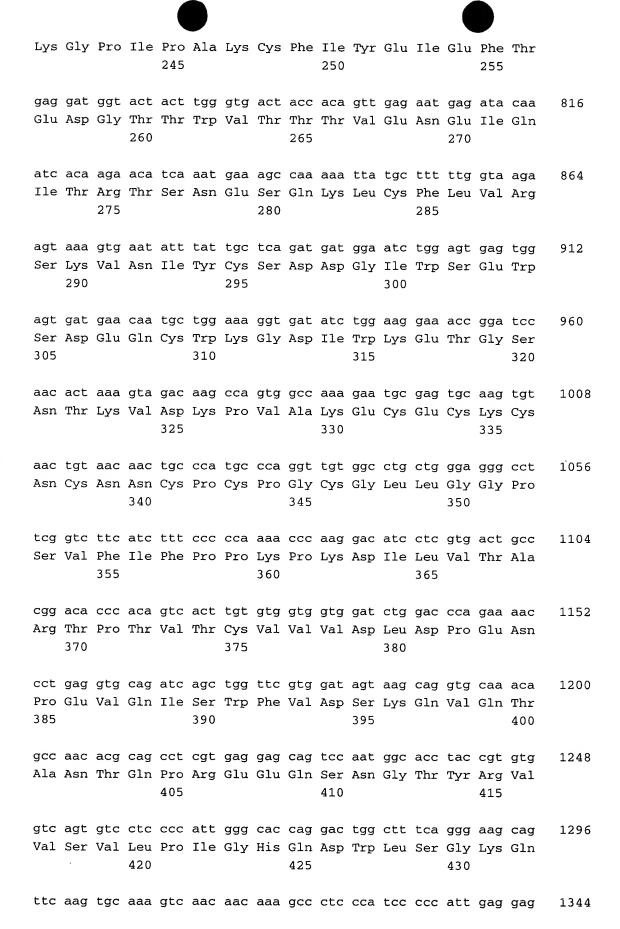
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  1
                  5
                                      10
                                                          15
ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg
                                                                    96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
             20
                                  25
                                                      30
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat
                                                                    144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35
                              40
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att
                                                                    192
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Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu 435 440 445 atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc 1392 Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val 450 455 ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr 465 470 475 tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag 1488 Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln 485 490 495 age aat gga cag gag cet gag age aag tae ege atg ace eeg eee Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro 500 cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg 1584 Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val 515 520 525 gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg 1632 Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met 530 535 540 cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct 1680 His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser 545 550 555 560 ccg ggt aaa tga 1692 Pro Gly Lys <210> 78 <211> 563 <212> PRT <213> Canis familiaris <400> 78 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp

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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr

25

20

35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser 145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys 180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile 195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser 210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro 225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr 245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln 260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg 275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp

290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met 

His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser

Pro Gly Lys

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<210> 79
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<211> 1692

<212> DNA

<213> Canis familiaris

## <400> 79

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catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
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                                                                  1692
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<211> 1686

<212> DNA

<213> Canis familiaris

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					gat Asp			-			_	144
					att Ile 55				-			192
					aaa Lys							240
					ctt Leu			_				288
			-		 gca Ala	_						336
					att Ile			-	-			384
					tct Ser 135							432
					ttt Phe							480
					atc Ile							528

165 170 175

			gag Glu				-			_	576
			gaa Glu								624
			ata Ile								672
			tca Ser 230						_		720
	_		gcc Ala					_			768
_			tgg Trp			-					816
			aat Asn				-	_	-	_	864
			tat Tyr					 -			912
			tgg Trp 310								960
			aag Lys								1008
			gtc Val						_		1056
			ccc Pro					_			1104

gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg 115 Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val

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aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc 1344

Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser

435

440

445

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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
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tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg 1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465 470 480

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Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn

485

490

495

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Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
515 520 525

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aaa tga Lys

<210> 81

<211> 561

<212> PRT

<213> Canis familiaris

<400> 81

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Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
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Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
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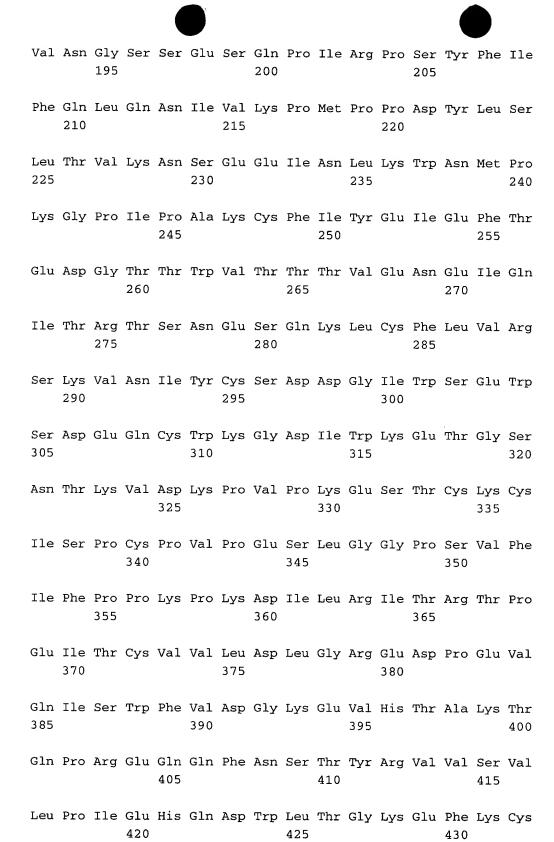
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Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys 180 185 190



440

435

Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser

445

Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro 450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu 465 470 475 480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn 485 490 495

Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu 500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys 515 520 525

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Lys

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<212> DNA

<213> Canis familiaris

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agacat
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<210> 83
<211> 29
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
<223> At locations 9, 18, 21 and 27, n = unknown

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athtggacnt ggaayccncc ngarggngc 29

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<210> 85

35

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<211> 45
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<220>
<223> At locations 7, 16, 25 and 40, n = unknown
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                                                                   45
<210> 88
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	<210>	89	
	<211>	53	
Ì	<212>	DNA	
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]			
2	<220>		
] :-	<223>	Description of Artificial Sequence: Synthetic	
		Primer	
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•	<400>	89	
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= = =			
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## Primer

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	<400> 92			
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	<211> 31			
ļ L	<212> DN	A		
	<213> Ar	tificial Sequence		
	<220>			
their their their a time		scription of Artificial Sequence: imer	Synthetic	
ļ 1	<400> 93	•		
į		ca acactaaagt agacaagcgt g		31
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	<211> 33			
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	Pr	imer		
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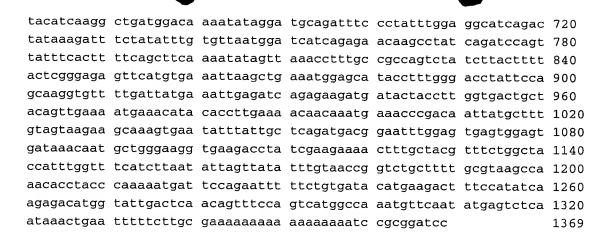
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gatcctggat tacttggtta tctctatttg caatggaaac ctcctgtggt tatagaaaaa 420
tttaagggct gtacactaga atatgagtta aaataccgaa atgttgatag cgacagctgg 480
aagactataa ttactaggaa tctaatttac aaggatgggt ttgatcttaa taaaqqcatt 540
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ccatggatag aagcttctta tgggatatca gatgaaggaa gtttggaaac taaaattcag 660
gacatgaagt gtatatatta taactggcag tatttggtct gctcttggaa acctggcaag 720
acagtatatt ctgataccaa ctataccatg tttttctggt atgagggctt ggatcatgcc 780
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tcctgggagt ctgccacaga caaaaacgat atgaagttga agaggagagc aaatgaaagt 1140
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tggagcgaat ggagtgaaga ggaatgttgg gaaggttaca cagggccaga ctcaaagatt 1260
attiticatag taccagitig ictiticiti ataticciti tqttactici tiqccitati 1320
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tgtgcttatg aagataccct ctgttaaacc accaatttct tgacatagag ccagccagca 1440
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aaaaaaaaa aaaaaaaaac tcgag
                                                               1525
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<211> 1369
<212> DNA
<213> Canis familiaris
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## <400> 96

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<400> 97

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gtcttcatgt atcacagaaa aattctggaa tcatttttgg gtaggtgttt ggcttacgca 180
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gtagcaaagt tttcttcgat aggtcttcac cttcccagca ttgtttatca ctccactcac 300
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aagccatttc teegagattt aaaacettga tattgeetet eteeeegeeg acaggcacae 1320
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<213> Artificial Sequence
<220>
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<211> 27
<212> DNA
<213> Artificial Sequence
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<223>	Description of Artificial Primer	Sequence:	Synthetic	
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ageous	aggacaca caucgeg			۷,
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	Primer			
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	Description of Artificial	Semience:	Synthetic	
	Primer	bequesies.	o y memocre	
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000	•			
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- <211> 21
- <212> DNA
- <213> Artificial Sequence
- <220>
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21